1645

#33

1600

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RAW SEQUENCE LISTING              DATE: 07/30/2002
PATENT APPLICATION:  US/09/044,696B   TIME: 15:11:26

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07302002\I044696B.raw
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 3 <110> APPLICANT: BARCHFELD, Gail
 4        DEL GIUDICE, Giuseppe
 5        RAPPUOLI, Rino
 7 <120> TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL ADP-RIBOSYLATING TOXINS
 8        AS PARENTERAL ADJUVANTS
10 <130> FILE REFERENCE: 2302-1393 / PP01393.002
12 <140> CURRENT APPLICATION NUMBER: 09/044,696B
13 <141> CURRENT FILING DATE: 1998-03-18
15 <160> NUMBER OF SEQ ID NOS: 5
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 711
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
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25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(708)
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type Subunit
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32 <400> SEQUENCE: 1
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34 Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
35   1               5                  10                  15
37 aaa cgt ttc cgg agt ctt atg ccc aga ggt aat gag tac ttc gat aga     96
38 Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
39              20                  25                  30
41 gga act caa atg aat att aat ctt tat gat cac gcg aga gga aca caa    144
42 Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
43              35                  40                  45
45 acc ggc ttt gtc aga tat gat gac gga tat gtt tcc act tct ctt agt    192
46 Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
47        50                  55                  60
49 ttg aga agt gct cac tta gca gga cag tat ata tta tca gga tat tca    240
50 Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
51  65                  70                  75                  80
53 ctt act ata tat atc gtt ata gca aat atg ttt aat gtt aat gat gta    288
54 Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
55                  85                  90                  95
57 att agc gta tac agc cct cac cca tat gaa cag gag gtt tct gcg tta    336
58 Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
59                 100                 105                 110
61 ggt gga ata cca tat tct cag ata tat gga tgg tat cgt gtt aat ttt    384
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Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\07302002\I044696B.raw**

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62 Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
63         115                 120                 125
65 ggt gtg att gat gaa cga tta cat cgt aac agg gaa tat aga gac cgg    432
66 Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
67         130                 135                 140
69 tat tac aga aat ctg aat ata gct ccg gca gag gat ggt tac aga tta    480
70 Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
71 145                 150                 155                 160
73 gca ggt ttc cca ccg gat cac caa gct tgg aga gaa gaa ccc tgg att    528
74 Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
75                 165                 170                 175
77 cat cat gca cca caa ggt tgt gga gat tca tca aga aca atc aca ggt    576
78 His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
79         180                 185                 190
81 gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc agg    624
82 Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
83         195                 200                 205
85 gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag tca    672
86 Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
87         210                 215                 220
89 gag gtt gac ata tat aac aga att cgg gat gaa tta tga                711
90 Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
91 225                 230                 235
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95 <211> LENGTH: 236
96 <212> TYPE: PRT
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type Subunit
101     A from E. coli heat labile toxin
103 <400> SEQUENCE: 2
104 Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
105   1               5                 10                 15
107 Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
108             20                 25                 30
110 Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
111         35                 40                 45
113 Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
114       50                 55                 60
116 Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
117 65                 70                 75                 80
119 Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
120                 85                 90                 95
122 Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
123             100                 105                 110
125 Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
126         115                 120                 125
128 Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
129         130                 135                 140
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RAW SEQUENCE LISTING   DATE: 07/30/2002
PATENT APPLICATION: US/09/044,696B   TIME: 15:11:26

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07302002\I044696B.raw

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131 Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
132 145               150               155               160
134 Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
135               165               170               175
137 His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
138               180               185               190
140 Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
141           195               200               205
143 Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
144       210               215               220
146 Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
147 225               230               235
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 723
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (1)..(720)
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type CT
161         subunit A
163 <400> SEQUENCE: 3
164 aat gat gat aag tta tat cgg gca gat tct aga cct cct gat gaa ata   48
165 Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
166  1               5                   10                  15
168 aag cag tca ggt ggt ctt atg cca aga gga cag agt gag tac ttt gac   96
169 Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
170               20                  25                  30
172 cga ggt act caa atg aat atc aac ctt tat gat cat gca aga gga act  144
173 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
174           35                  40                  45
176 cag acg gga ttt gtt agg cac gat gat gga tat gtt tcc acc tca att  192
177 Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
178       50                  55                  60
180 agt ttg aga agt gcc cac tta gtg ggt caa act ata ttg tct ggt cat  240
181 Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
182 65                  70                  75                  80
184 tct act tat tat ata tat gtt ata gcc act gca ccc aac atg ttt aac  288
185 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
186               85                  90                  95
188 gtt aat gat gta tta ggg gca tac agt cct cat cca gat gaa caa gaa  336
189 Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
190               100               105               110
192 gtt tct gct tta ggt ggg att cca tac tcc caa ata tat gga tgg tat  384
193 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
194           115               120               125
196 cga gtt cat ttt ggg gtg ctt gat gaa caa tta cat cgt aat agg ggc  432
197 Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
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RAW SEQUENCE LISTING   DATE: 07/30/2002
PATENT APPLICATION: US/09/044,696B   TIME: 15:11:26

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07302002\I044696B.raw

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198     130                    135                    140
200 tac aga gat aga tat tac agt aac tta gat att gct cca gca gca gat    480
201 Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
202 145                    150                    155                    160
204 ggt tat gga ttg gca ggt ttc cct ccg gag cat aga gct tgg agg gaa    528
205 Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
206                    165                    170                    175
208 gag ccg tgg att cat cat gca ccg ccg ggt tgt ggg aat gct cca aga    576
209 Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
210                    180                    185                    190
212 tca tcg atc agt aat act tgc gat gaa aaa acc caa agt cta ggt gta    624
213 Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
214         195                    200                    205
216 aaa ttc ctt gac gaa tac caa tct aaa gtt aaa aga caa ata ttt tca    672
217 Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
218         210                    215                    220
220 ggc tat caa tct gat att gat aca cat aat aga att aag gat gaa tta    720
221 Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
222 225                    230                    235                    240
224 tga                                                                  723
227 <210> SEQ ID NO: 4
228 <211> LENGTH: 240
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type CT
234        subunit A
236 <400> SEQUENCE: 4
237 Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
238   1               5                    10                    15
240 Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
241             20                    25                    30
243 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
244         35                    40                    45
246 Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
247     50                    55                    60
249 Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
250 65                    70                    75                    80
252 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
253                    85                    90                    95
255 Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
256             100                    105                    110
258 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
259         115                    120                    125
261 Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
262     130                    135                    140
264 Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
265 145                    150                    155                    160
267 Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
```

```
268                  165                 170                 175
270 Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
271              180                 185                 190
273 Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
274          195                 200                 205
276 Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
277      210                 215                 220
279 Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
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284 <211> LENGTH: 240
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type Subunit
290       A from E. coli heat labile toxin
292 <400> SEQUENCE: 5
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294 1               5                   10                  15
296 Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr Phe Asp
297              20                  25                  30
299 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
300          35                  40                  45
302 Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu
303      50                  55                  60
305 Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser Gly Tyr
306 65               70                  75                  80
308 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
309              85                  90                  95
311 Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu Gln Glu
312              100                 105                 110
314 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
315          115                 120                 125
317 Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
318      130                 135                 140
320 Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
321 145              150                 155                 160
323 Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
324              165                 170                 175
326 Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
327              180                 185                 190
329 Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
330          195                 200                 205
332 Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
333      210                 215                 220
335 Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
336 225              230                 235                 240
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VERIFICATION SUMMARY DATE: 07/30/2002
PATENT APPLICATION: **US/09/044,696B** TIME: 15:11:27

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\07302002\I044696B.raw**